

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/635,130ADATE: 09/18/98
TIME: 08:24:25

INPUT SET: S28724.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: Caras, Ingrid W

(ii) TITLE OF INVENTION: A2-1 Neurotrophic Factor

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Genentech, Inc.

(B) STREET: 1 DNA Way

(C) CITY: South San Francisco

(D) STATE: California

(E) COUNTRY: USA

(F) ZIP: 94080

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: WinPatin (Genentech)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/635130

(B) FILING DATE: 19-Mar-1996

(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Torchia, PhD., Timothy E.

(B) REGISTRATION NUMBER: 36,700

(C) REFERENCE/DOCKET NUMBER: P1001

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650/225-8674

(B) TELEFAX: 650/952-9881

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1877 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(ix) FEATURE:

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/635,130ADATE: 09/18/98
TIME: 08:24:26

INPUT SET: S28724.raw

47 (A) NAME/KEY: Extra Cellular Domain
48 (B) LOCATION: 244-899
49 (C) IDENTIFICATION METHOD:
50 (D) OTHER INFORMATION:
51
52 (ix) FEATURE:
53 (A) NAME/KEY: Transmembrane Domain
54 (B) LOCATION: 901-978
55 (C) IDENTIFICATION METHOD:
56 (D) OTHER INFORMATION:
57
58 (ix) FEATURE:
59 (A) NAME/KEY: signal peptide
60 (B) LOCATION: 244-321
61 (C) IDENTIFICATION METHOD:
62 (D) OTHER INFORMATION:
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66
67 GNTCTAGAAN TAGTGGATCC CCCCGGGCTG CAGGAATTCC GACGGCCCCCT 50
68
69 GGAAGGGCTC TGGTGGGGCT GAGCGCTCTG CCGCGGGGGC GCGGGCACAG 100
70
71 CAGGAAGCAG GTCCGCGTGG GCGCTGGGGG CATCAGCTAC CGGGGTGGTC 150
72
73 CGGGCTGAAG AGCCAGGCAG CCAAGGCAGC CACCCCGGGG GGTGGGCGAC 200
74
75 TTTGGGGGAG TTGGTGCCCC GCCCCCAGG CCTTGGCGGG GTC ATG 246
76 Met
77 1
78
79 GGG CCC CCC CAT TCT GGG CCG GGG GGC GTG CGA GTC GGG 285
80 Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly
81 5 10
82
83 GCC CTG CTG CTG CTG GGG GTT TTG GGG CTG GTG TCT GGG 324
84 Ala Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly
85 15 20 25
86
87 CTC AGC CTG GAG CCT GTC TAC TGG AAC TCG GCG AAT AAG 363
88 Leu Ser Leu Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys
89 30 35 40
90
91 AGG TTC CAG GCA GAG GGT GGT TAT GTG CTG TAC CCT CAG 402
92 Arg Phe Gln Ala Glu Gly Gly Tyr Val Leu Tyr Pro Gln
93 45 50
94
95 ATC GGG GAC CGG CTA GAC CTG CTC TGC CCC CGG GCC CGG 441
96 Ile Gly Asp Arg Leu Asp Leu Leu Cys Pro Arg Ala Arg
97 55 60 65
98
99 CCT CCT GGC CCT CAC TCC TCT CCT AAT TAT GAG TTC TAC 480

RAW SEQUENCE LISTING PATENT APPLICATION US/08/635,130A

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100  Pro Pro Gly Pro His Ser Ser Pro Asn Tyr Glu Phe Tyr
101              70              75
102
103  AAG CTG TAC CTG GTA GGG GGT GCT CAG GGC CGG CGC TGT 519
104  Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg Arg Cys
105      80              85              90
106
107  GAG GCA CCC CCT GCC CCA AAC CTC CTT CTC ACT TGT GAT 558
108  Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp
109              95              100              105
110
111  CGC CCA GAC CTG GAT CTC CGC TTC ACC ATC AAG TTC CAG 597
112  Arg Pro Asp Leu Asp Leu Arg Phe Thr Ile Lys Phe Gln
113              110              115
114
115  GAG TAT AGC CCT AAT CTC TGG GGC CAC GAG TTC CGC TCG 636
116  Glu Tyr Ser Pro Asn Leu Trp Gly His Glu Phe Arg Ser
117      120              125              130
118
119  CAC CAC GAT TAC TAC ATC ATT GCC ACA TCG GAT GGG ACC 675
120  His His Asp Tyr Tyr Ile Ile Ala Thr Ser Asp Gly Thr
121              135              140
122
123  CGG GAG GGC CTG GAG AGC CTG CAG GGA GGT GTG TGC CTA 714
124  Arg Glu Gly Leu Glu Ser Leu Gln Gly Gly Val Cys Leu
125      145              150              155
126
127  ACC AGA GGC ATG AAG GTG CTT CTC CGA GTG GGA CAA AGT 753
128  Thr Arg Gly Met Lys Val Leu Leu Arg Val Gly Gln Ser
129              160              165              170
130
131  CCC CGA GGA GGG GCT GTC CCC CGA AAA CCT GTG TCT GAA 792
132  Pro Arg Gly Gly Ala Val Pro Arg Lys Pro Val Ser Glu
133              175              180
134
135  ATG CCC ATG GAA AGA GAC CGA GGG GCA GCC CAC AGC CTG 831
136  Met Pro Met Glu Arg Asp Arg Gly Ala Ala His Ser Leu
137      185              190              195
138
139  GAG CCT GGG AAG GAG AAC CTG CCA GGT GAC CCC ACC AGC 870
140  Glu Pro Gly Lys Glu Asn Leu Pro Gly Asp Pro Thr Ser
141              200              205
142
143  AAT GCA ACC TCC CGG GGT GCT GAA GGC CCC CTG CCC CCT 909
144  Asn Ala Thr Ser Arg Gly Ala Glu Gly Pro Leu Pro Pro
145      210              215              220
146
147  CCC AGC ATG CCT GCA GTG GCT GGG GCA GCA GGG GGG CTG 948
148  Pro Ser Met Pro Ala Val Ala Gly Ala Ala Gly Gly Leu
149              225              230              235
150
151  GCG CTG CTC TTG CTG GGC GTG GCA GGG GCT GGG GGT GCC 987
152  Ala Leu Leu Leu Leu Gly Val Ala Gly Ala Gly Gly Ala

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153		240		245	
154					
155	ATG TGT TGG CGG AGA CGG CGG GCC AAG CCT TCG GAG AGT				1026
156	Met Cys Trp Arg Arg Arg Arg Ala Lys Pro Ser Glu Ser				
157	250		255		260
158					
159	CGC CAC CCT GGT CCT GGC TCC TTC GGG AGG GGA GGG TCT				1065
160	Arg His Pro Gly Pro Gly Ser Phe Gly Arg Gly Gly Ser				
161		265		270	
162					
163	CTG GGC CTG GGG GGT GGA GGT GGG ATG GGA CCT CGG GAG				1104
164	Leu Gly Leu Gly Gly Gly Gly Gly Met Gly Pro Arg Glu				
165	275		280		285
166					
167	GCT GAG CCT GGG GAG CTA GGG ATA GCT CTG CGG GGT GGC				1143
168	Ala Glu Pro Gly Glu Leu Gly Ile Ala Leu Arg Gly Gly				
169		290		295	300
170					
171	GGG GCT GCA GAT CCC CCC TTC TGC CCC CAC TAT GAG AAG				1182
172	Gly Ala Ala Asp Pro Pro Phe Cys Pro His Tyr Glu Lys				
173		305		310	
174					
175	GTG AGT GGT GAC TAT GGG CAT CCT GTG TAT ATC GTG CAG				1221
176	Val Ser Gly Asp Tyr Gly His Pro Val Tyr Ile Val Gln				
177		315		320	325
178					
179	GAT GGG CCC CCC CAG AGC CCT CCA AAC ATC TAC TAC ACA				1260
180	Asp Gly Pro Pro Gln Ser Pro Pro Asn Ile Tyr Tyr Thr				
181		330		335	
182					
183	TCG ATT TCT GTG TTG GAG TGG CCC ATA TTG CAT ACG ATA				1299
184	Ser Ile Ser Val Leu Glu Trp Pro Ile Leu His Thr Ile				
185	340		345		350
186					
187	CAA CTG TTT TTC ATG CGA TCC AAG TGC TCC CGT GTC ACT				1338
188	Gln Leu Phe Phe Met Arg Ser Lys Cys Ser Arg Val Thr				
189		355		360	365
190					
191	ACA TTC TTA TTT CCT GTG CAA GTT ATT ACG ACA TCG ACT				1377
192	Thr Phe Leu Phe Pro Val Gln Val Ile Thr Thr Ser Thr				
193		370		375	
194					
195	TGC CGG ATG ACT TCA TTT AGC TTT ACC ACC CTG AAC CCA				1416
196	Cys Arg Met Thr Ser Phe Ser Phe Thr Thr Leu Asn Pro				
197		380		385	390
198					
199	TCC ATG CAG GCC TGC AGA GCA CAG ATG GGG GAA TTC CGA				1455
200	Ser Met Gln Ala Cys Arg Ala Gln Met Gly Glu Phe Arg				
201		395		400	
202					
203	ATC AGA TGG TGT TTC TGG GGG GAC AGG ATC CTG GGT ACG				1494
204	Ile Arg Trp Cys Phe Trp Gly Asp Arg Ile Leu Gly Thr				
205	405		410		415

RAW SEQUENCE LISTING
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206
207 GCT CTG TTT GTG CTT GTG CTT ATT CTT CTT CTT GGG AGG 1533
208 Ala Leu Phe Val Leu Val Leu Ile Leu Leu Leu Gly Arg
209 420 425 430
210
211 CTG AAT ATG CAT CAG ACG ACA CTG CTC CGG CAA CGG GCC 1572
212 Leu Asn Met His Gln Thr Thr Leu Leu Arg Gln Arg Ala
213 435 440
214
215 AGT GTG GAG GCG GAA GCC GGC CAG CAT GGT CCC CTG TG 1610
216 Ser Val Glu Ala Glu Ala Gly Gln His Gly Pro Leu
217 445 450 455
218
219 ATAGGATTGA AAGAGCTACT GAGAATAGGG GGCTTCTCAA TGAGAGAGCG 1660
220
221 GAGGCTGCTG TTATCATGGG AACCAGGCAG ATCAATCATC CCTGGCAGGT 1710
222
223 CAGGCAGGAA GTTACTTAGC TTCTCCTTCA CCTTCTTCCC ACAGAATTTA 1760
224
225 TTATAGGCTT GTTCCAAGTT GTAGTGTGTG ATCAGATTCG TGCTGCCTGT 1810
226
227 CAGCTCTGTG CTACCTGGCA GTTCCCCTCA TGAATTCTGA TATCAAGCTT 1860
228
229 ATCGATACCG TCGACCT 1877
230
231 (2) INFORMATION FOR SEQ ID NO:2:
232
233 (i) SEQUENCE CHARACTERISTICS:
234 (A) LENGTH: 455 amino acids
235 (B) TYPE: Amino Acid
236 (D) TOPOLOGY: Linear
237
238 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
239
240 Met Gly Pro Pro His Ser Gly Pro Gly Gly Val Arg Val Gly Ala
241 1 5 10 15
242
243 Leu Leu Leu Leu Gly Val Leu Gly Leu Val Ser Gly Leu Ser Leu
244 20 25 30
245
246 Glu Pro Val Tyr Trp Asn Ser Ala Asn Lys Arg Phe Gln Ala Glu
247 35 40 45
248
249 Gly Gly Tyr Val Leu Tyr Pro Gln Ile Gly Asp Arg Leu Asp Leu
250 50 55 60
251
252 Leu Cys Pro Arg Ala Arg Pro Pro Gly Pro His Ser Ser Pro Asn
253 65 70 75
254
255 Tyr Glu Phe Tyr Lys Leu Tyr Leu Val Gly Gly Ala Gln Gly Arg
256 80 85 90
257
258 Arg Cys Glu Ala Pro Pro Ala Pro Asn Leu Leu Leu Thr Cys Asp

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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/635,130A

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Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: 08/635130